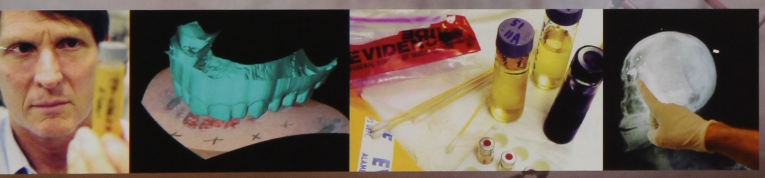
THE NEW FORENSIC SCIENCE



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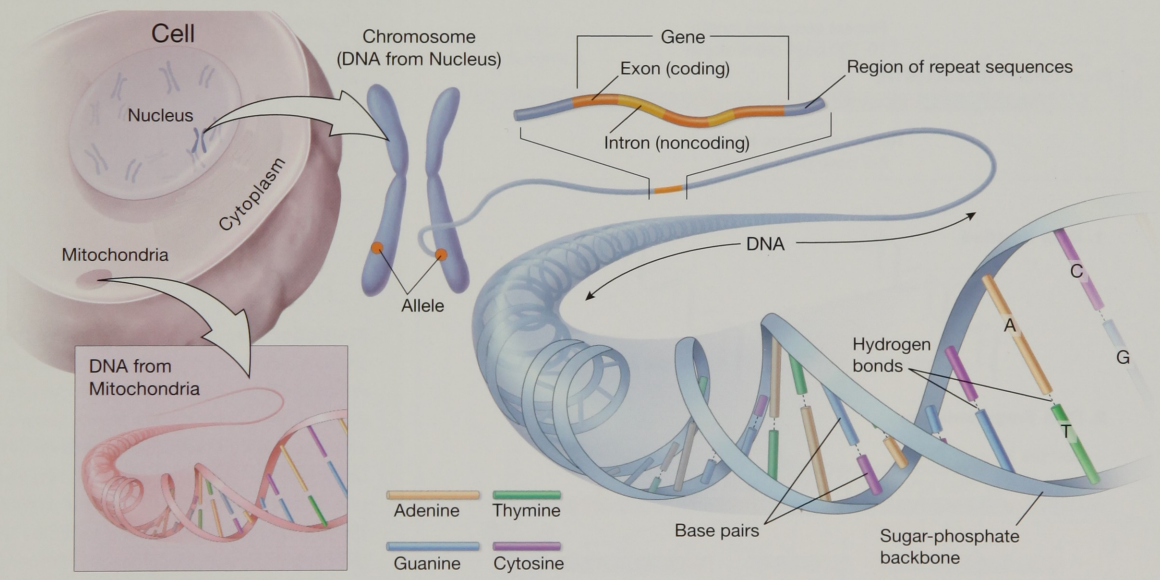
FORENSIC VIEWS OF THE BODY

FORENSIC DNA

HOW DOES DNA HELP SOLVE CRIMES?

In February of 1953, the journal *Nature* published a slim paper that would forever change the study of biology. In it, the young scientists James Watson and Francis Crick became the first to describe the molecule at the heart of inheritance, known as deoxyribonucleic acid, or DNA. The secret to DNA's singular role in life, they explained, is its structure: Each molecule is an elegant strand in the form of a "double helix," a configuration that allows DNA to "unzip" and be copied, ad infinitum.

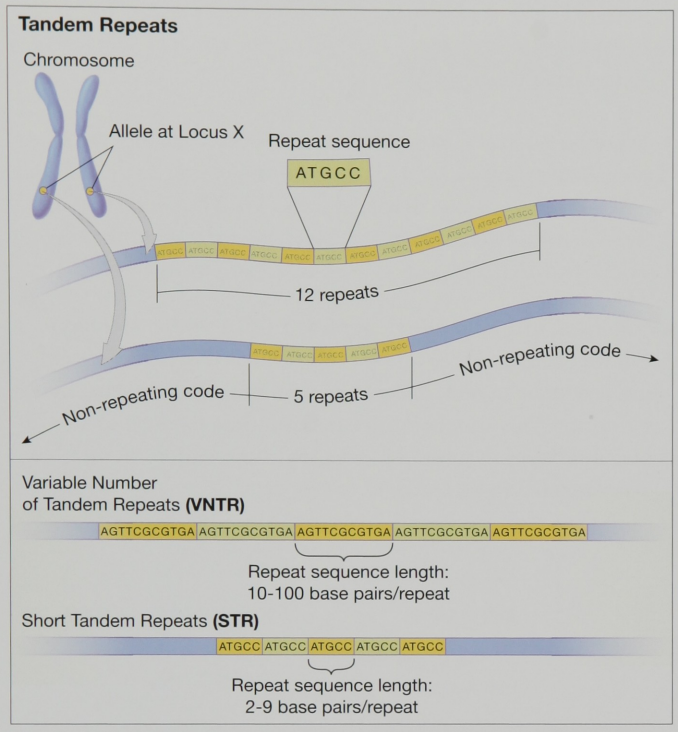
When, two decades later, scientists became able to amplify tiny samples of DNA with a technique called Polymerase Chain Reaction (PCR), the study of DNA and its role in individual differences became much easier. In the decades since, scientists have developed a series of techniques that allow them to profile an individual's genetic blueprint. These techniques have countless medical uses, but they have also become indispensable crime-fighting tools because they allow biological samples collected from crime scenes or other environments to be matched to suspects.



DNA

DNA stores biological information in sequences of four bases of nucleic acid—adenine (A), thymine (T), cytosine (C) and guanine (G)—which are strung along ribbons of sugar-phosphate molecules in the shape of a double helix. Because each base will only form hydrogen bonds across the helix with its opposing base (A with T, and C with G), an unzipped DNA molecule creates two templates for exact copies.

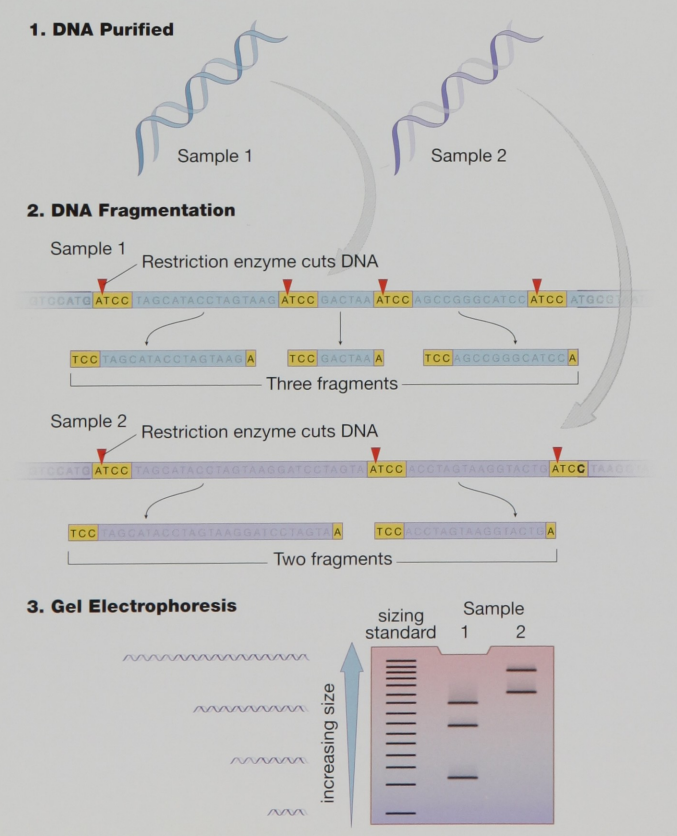
Every cell in the human body carries a bundle of DNA in its nucleus—about three billion chemical nucleotides encoding roughly 30,000 genes, discrete chunks of DNA that are translated into individual proteins. Each of the 46 chromosomes in a human cell's nucleus bears thousands of genes. Chromosomes come in pairs, one from each parent, a given gene is represented by two variants, known as alleles. Taken as a whole, this package of DNA serves as its owner's complete genetic blueprint. Just as no two humans are alike, no two blueprints—except those belonging to identical twins—are, either.



VNTR

The full genetic profiles of any two individuals (other than identical twins) reveal many differences. But since most human genes are the same from person to person, DNA typing relies on the stretches of DNA that tend to differ among different people. While the repeated sequences themselves are usually the same from person to person, the number of times they are repeated tends to vary.

These stretches of repeats, known as Variable Number of Tandem Repeats or VNTRs, can be isolated from an individual's DNA. The number of repeats can be gauged by dividing the entire molecular weight of a given VNTR by the molecular weight of the repeated sequence. VNTRs are similar to Short Tandem Repeats (For more on STRs, see page 3), the difference being that in a VNTR, the repeated sequence is longer—about 10-100 base pairs long.



RFLP

Restriction Fragment Length Polymorphism (RFLP) analysis measures fragments of DNA containing short sequences that vary from person to person, called VNTRs. After extracting DNA from a sample and amplifying it with the technique known as Polymerase Chain Reaction (See page 4), a technician adds restriction enzymes that cut the DNA at specific points. The resulting fragments can be sorted by length with gel electrophoresis technology to determine how many times a given VNTR is repeated.

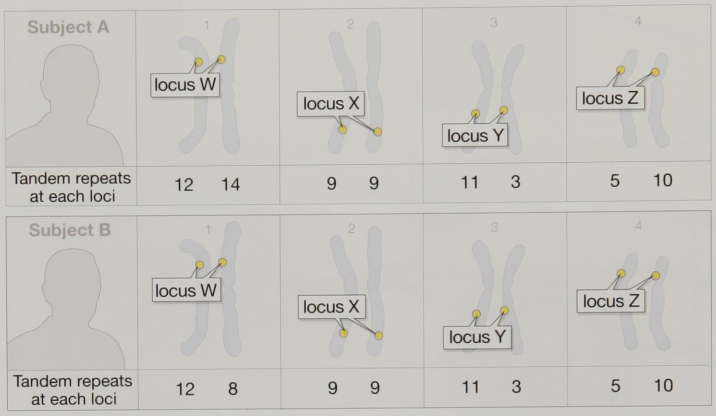
If two different samples show VNTRs of different lengths, the samples could not have come from the same person. On the other hand, two samples showing VNTRs of the same length could have come from the same person, or from two people who happen to have VNTRs of the same length at that location. By comparing enough VNTRs from two individuals, however, the likelihood of a coincidental match can be reduced to nearly zero. RFLP testing requires hundreds of steps and weeks to complete, and it has been largely replaced by newer, faster techniques.

STR

A Short Tandem Repeat (STR) is a region of DNA composed of a short sequence of nucleotides repeated many times. Since the number of repeated sequences in a given STR varies from person to person, pinpointing these variants can be useful in DNA fingerprinting.

As the name implies, the repeated stretches in STRs are short—only two to ten base pairs long. For this reason, and because they are dispersed more evenly throughout the genome than the longer Variable Number of Tandem Repeats, or VNTRs, STRs are favored by forensic labs.

Large databases of information on STRs in the general population tell analysts how much variation exists at any given STR location. That information can help forensic analysts determine the conclusiveness of a "match" between two samples. If ten percent of people have the same number of repeats at a given STR, for example, finding a match at that site is merely suggestive that two samples are a match. If two sites with the same prevalence match, the odds drop to one in a hundred that the similarity is coincidental. If 13 sites match, the odds that any two people would possess such a fingerprint are so small— about one in ten trillion—that the result can be considered a definitive match.



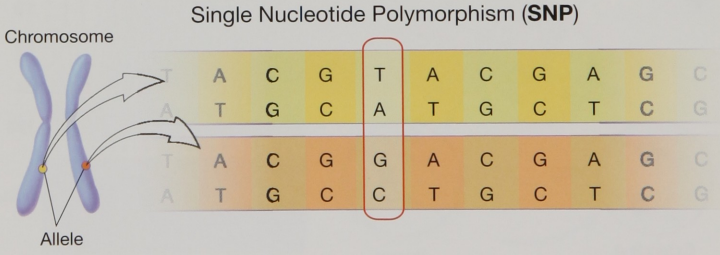
Results

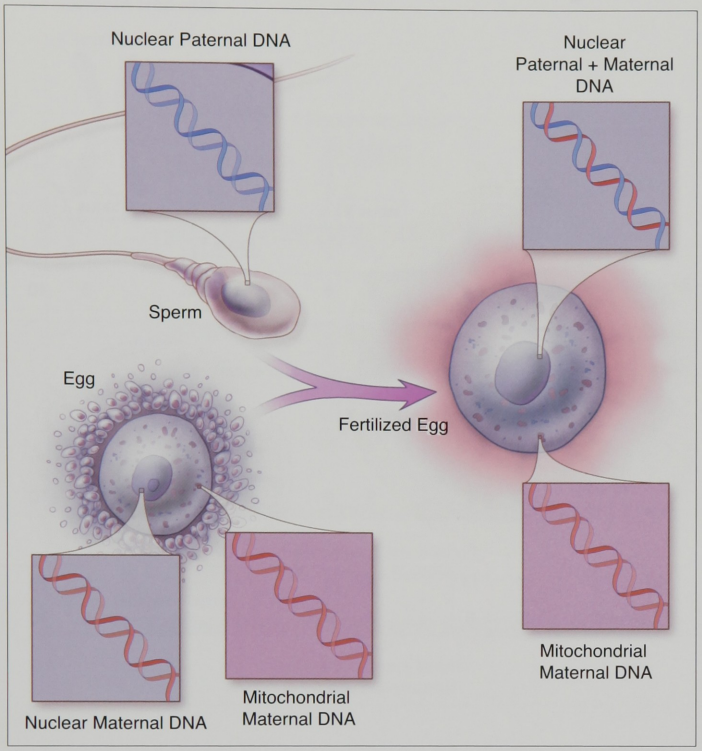
Subject A	12	14	9	9	11	3	5	10
Subject B	12	8	9	9	11	3	5	10

SNP

Single Nucleotide Polymorphisms or SNPs (pronounced "snips") are variations in a DNA sequence that occur when a single nucleotide in the sequence is different from the norm in at least one percent of the population. When SNPs occur inside a gene, they create different variants, or alleles, of that gene.

Unlike repeated portions of DNA like STRs and VNTRs, in the case of SNPs it is the sequence itself, not its length, that is useful to forensic scientists. SNPs are common, occurring every 100 to 300 bases along the entire length of the human genome. Mutations in SNPs are very rare, so the sequences tend to be passed unchanged across generations. But because any given SNP is relatively common in the population, an analyst must examine dozens of SNPs to derive a true DNA fingerprint. For this reason, SNP analysis is rarely used in forensic cases.

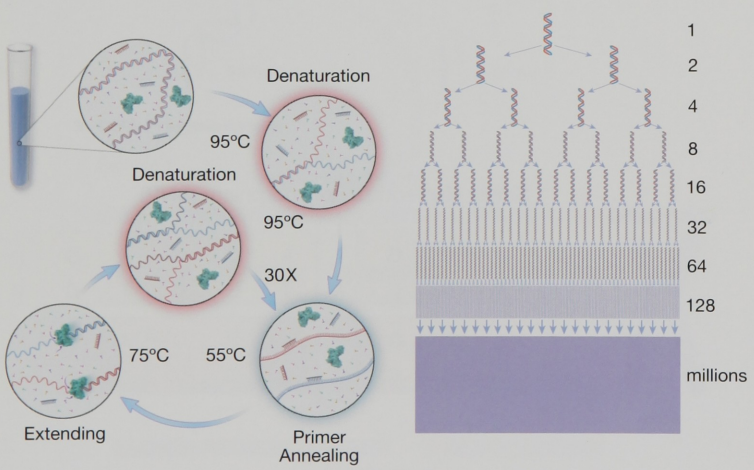




mtDNA

Most DNA is packed tightly into the cell's nucleus, but there is also a tiny loop of genetic material, called mitochondrial DNA (mtDNA), in a part of the cell known as the mitochondria. Each cell has only one nucleus, but there are hundreds of mitochondria in a given cell, each bearing a copy of the owner's mtDNA sequence. Because of its relative abundance in the cell, mtDNA can often be extracted from old or degraded samples in which nuclear DNA is sparse.

Comparing an individual's mtDNA profile with the profile of a potential maternal relative is particularly useful for identification, because mtDNA is inherited only from the mother. When an egg cell is fertilized, the 23 chromosomes from the nucleus of a sperm cell join the 23 chromosomes inside the egg. The egg cell's mtDNA remains unaffected, while the sperm's mtDNA is left behind.



PCR

Polymerase Chain Reaction, or PCR, is a simple yet essential way to make copies of a small amount of DNA by exploiting DNA's natural ability to replicate itself when a cell divides.

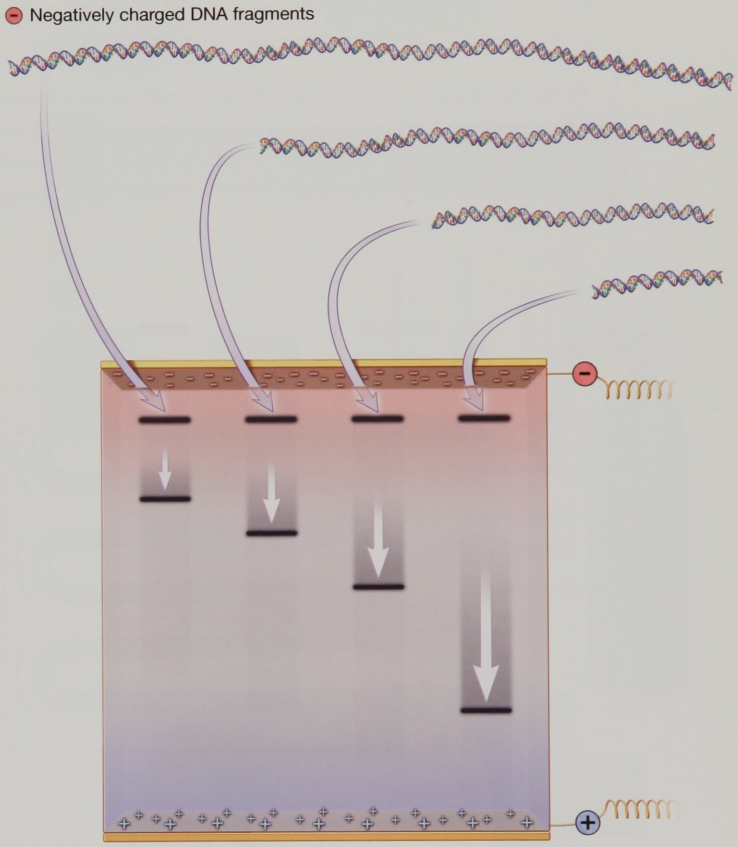
The first step is to extract a small amount of DNA from a sample taken from an individual or piece of evidence. The DNA is mixed with a chemical cocktail including natural enzymes, synthetic chemicals called primers, and the four nucleotides (adenine, thymine, cytosine and guanine). After filling tiny plastic tubes with the mixture, a technician places them in a microwave-sized machine that heats and cools the tubes to a series of precise temperatures.

The changing temperatures ignite a chain of events, beginning with the denaturing (unzipping) of the double-stranded DNA molecules. Next, the primers bind to the individual strands at precise locations, a process known as annealing. Ushered in place by the primers, enzymes steer the copying of long stretches of code. This sequence is repeated billions of times in just a few hours, supplying ample DNA for investigation.

Electrophoresis

Once DNA has been extracted from a sample and a section bearing useful code—such as a VNTR or STR (see pages 3 and 4)—is isolated, the next step in DNA fingerprinting is to measure each strand and count the number of repeated sections. To do this, scientists use a technique called gel electrophoresis, which uses an electric current to push strands of DNA through a slab of gel-like material.

Because each bit of DNA is negatively charged and subject to an equal electric force propelling it to the positively-charged side of the gel, smaller pieces move faster than larger ones. When the current is removed, the gel is photographed to reveal how far each bit has migrated. By comparing the bands produced by the DNA sample of interest with bands produced by "standard" samples whose sizes are already known, the precise length of each DNA fragment can be gauged.

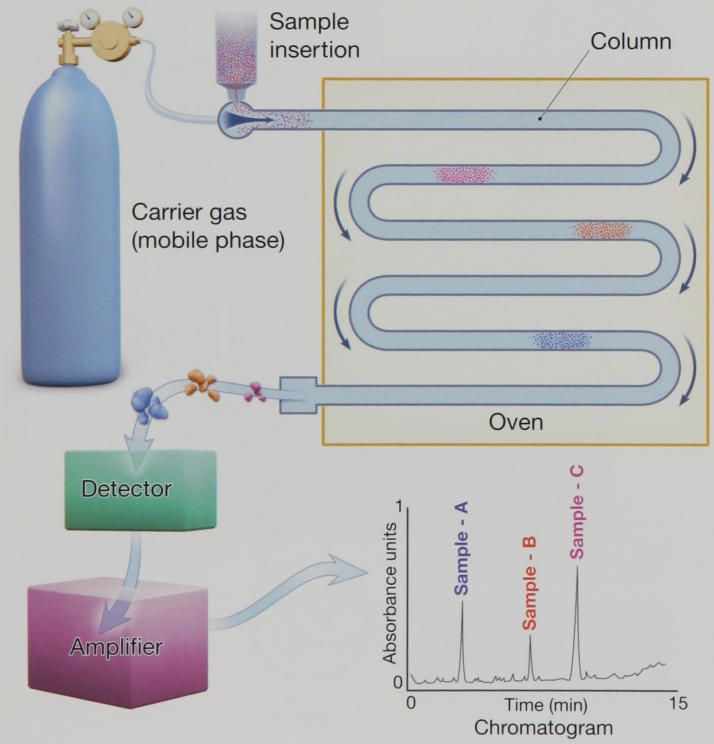


FORENSIC TOXICOLOGY

WHAT IS FORENSIC TOXICOLOGY?

When the Industrial Revolution ushered in the commercial production of a variety of dangerous chemicals, poisoning became an increasingly common crime. Since then, there has been a growing need to identify poisons and other substances — sometimes present in only minute quantities — involved in crimes, a field known as forensic toxicology. A mere trace of powder, for example, can help determine the cause of death in an instance of poisoning. Analyzing a single strand of hair sample can reveal a person's history of drug use.

As the techniques used to identify and study small chemical samples have been refined, forensic scientists have become increasingly able to analyze tiny samples. More often than not, the first step is to divide a chemical sample into its individual components. Once isolated, the chemical and physical properties of each component can be compared to a range of known samples for identification.



Gas Chromatography

Gas chromatography determines how many chemicals are present in a sample and separates each compound for further study. It works like this: First, the chromatography instrument vaporizes a small liquid sample inside a special chamber, sweeping the resulting gas through a heated column with the help of an inert carrier gas. This is known as the "mobile phase." A liquid "stationary phase" inside the column slows the sample gas molecules as they pass through the column.

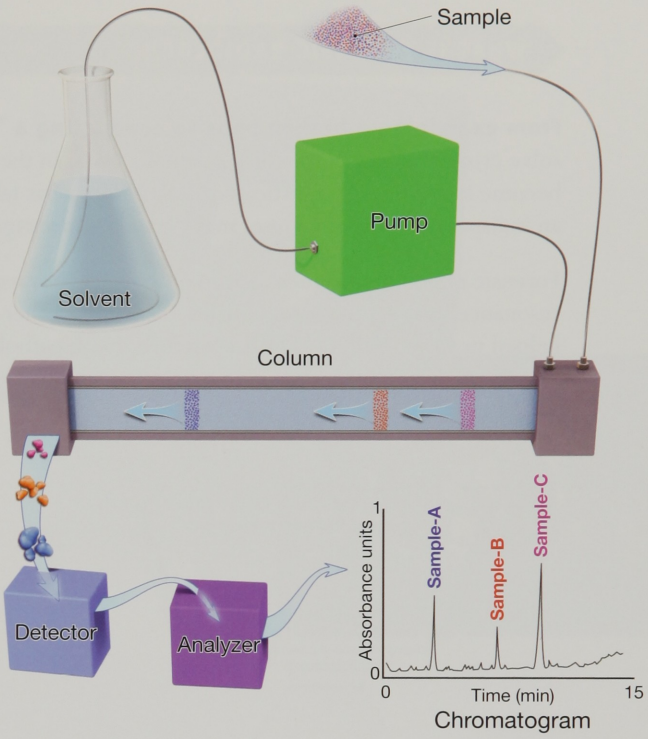
Depending on their size and other properties, different compounds pass through the stationary phase at different rates, emerging from the column one by one. Just before each compound exits the instrument, it passes through a detector that records the time and relative quantity of each substance.

The detector sends an electronic signal to an amplifier, which prints a chromatogram representing the exit time and amount of each compound with a series of peaks. Comparing these peaks to the patterns known to be produced by certain substances—narcotics, for example—offers clues to the composition of the original sample.

HPLC

High Performance Liquid Chromatography, or HPLC, helps determine the chemical composition of unknown mixed samples—such as those containing proteins—that can't be easily vaporized into a gas. A sample is first passed through a pressurized column containing a solvent that separates the sample's individual chemical components. Unlike gas chromatography, where the sample is vaporized before being passed through a column, in HPLC the sample stays in liquid form. As the different compounds emerge from the column, their transit times and relative concentrations are recorded by a detector.

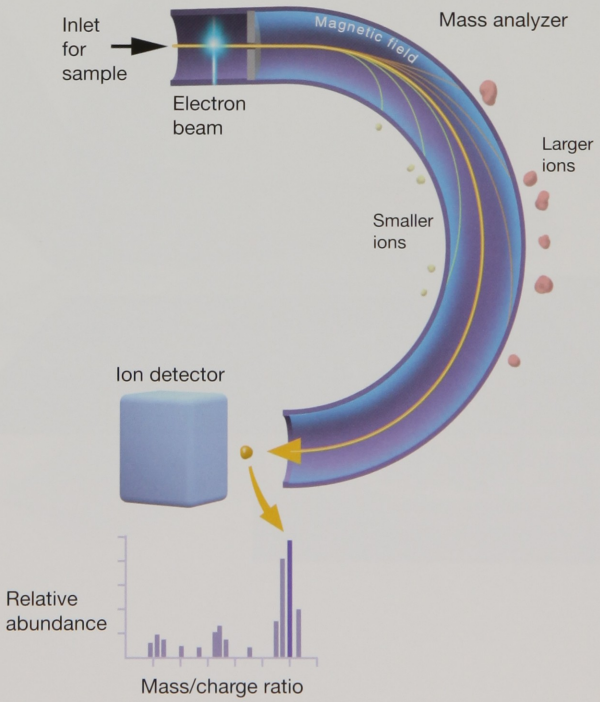
The printed results, or chromatogram, show each compound as a peak representing quantity and exit time. By comparing these peaks to the patterns shown by known substances, an analyst can often determine the chemical composition of the original sample.



Mass Spectrometry

While chromatography separates compounds depending on their chemical and physical properties, mass spectrometry—or mass spec, as it is commonly known—reveals a compound's molecular weight. In a mass spectrophotometer, a beam of electrons bombards a single chemical sample with enough energy to break apart molecules. The fragments produced are propelled through a magnetic field and automatically sorted according to their mass and charge. An ion detector collects and records the fragments, producing a graph showing the mass to charge ratio of each.

To analyze the information and deduce the structure of the original molecule, a scientist must work backwards, re-assembling the fragments on paper. When all goes well, they fit together like puzzle pieces to reveal the composition of the original sample.

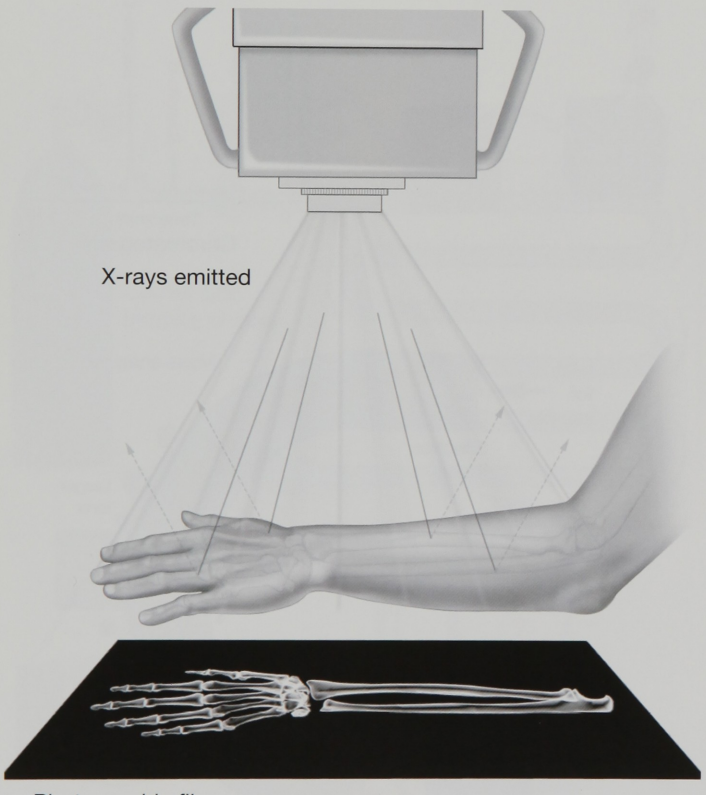


FORENSIC RADIOLOGY

WHAT IS FORENSIC RADIOLOGY?

From examining a broken bone to conducting a "virtual autopsy," forensic radiologists help solve crimes by looking at clues inside the body. In the last 20 years, as imaging techniques have become increasingly sophisticated and radiology has taken center stage in medicine, it has also become an indispensable component of many criminal investigations.

Forensic radiology includes the use of tools like X-rays, computed tomography and magnetic resonance imaging to reveal injuries, diseases or other abnormalities. In the field's early days, X-rays helped us to see bullets lodged in victims. Now, pathologists use radiographic images in autopsies to identify foreign bodies and determine causes of death.

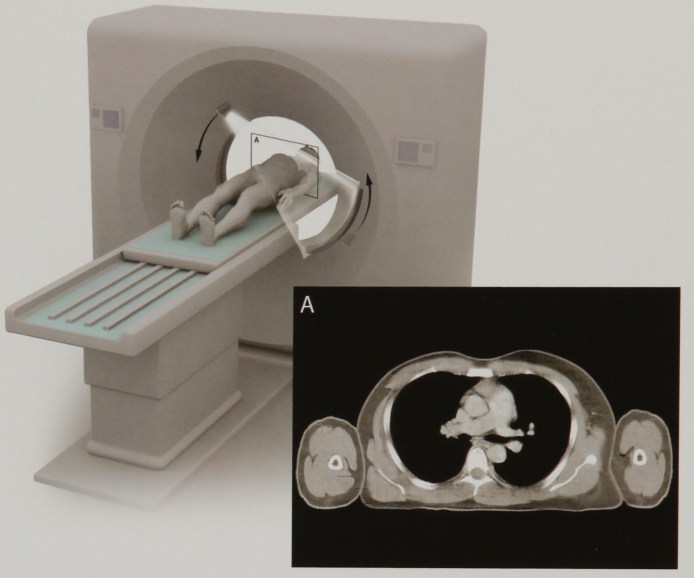


X-ray

Like visible light, X-rays are a form of electromagnetic energy carried by particles called photons. However, our eyes are only sensitive to a certain range of electromagnetic wavelengths, so we can see visible light but not shorter-wavelength X-rays or longer-wavelength radio waves. X-ray photons are high in energy, which means they can pass through materials that deflect light, including the body's soft tissue. Other materials that are composed of larger atoms—such as metals and the calcium atoms that make up bones—absorb X-ray photons. To capture an image of the body's interior, X-ray machines shine a beam of X-ray photons at a target, and the pattern of X-ray light is recorded on film after passing through the tissue.

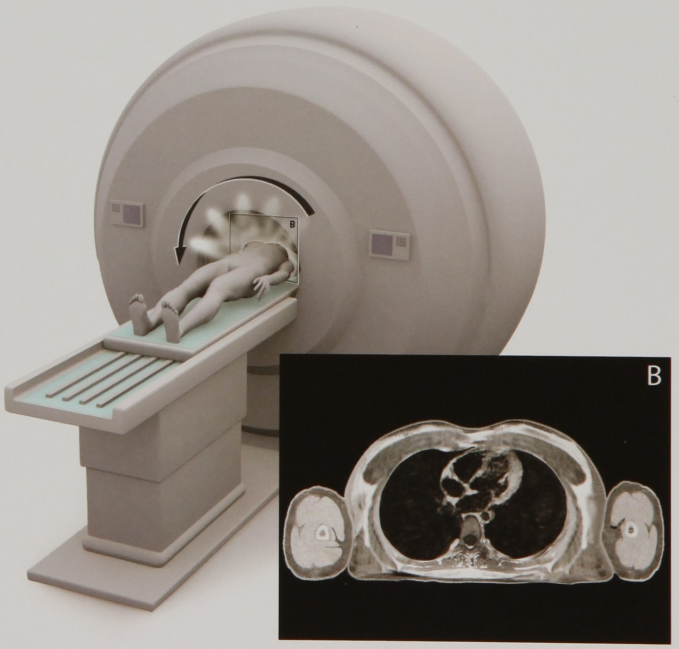
Computed Tomography

Computed axial tomography (also known as a CAT or CT scan) takes X-ray imaging a step further by creating a three-dimensional picture of the human body from a series of two-dimensional X-ray scans. It works like this: A patient generally lies on a flat bed that passes through the hollow middle of a device that looks like a giant square donut. A scanning apparatus rotates around the patient, aiming spirals of X-ray beams at whatever section of the body is being scanned. As the X-rays pass through the body, they are absorbed or weakened at different levels depending on the tissues they encounter. The result is a series of images and shadows that create an impression of bone and soft tissue. Sophisticated computer software interprets the X-ray shadows from many angles, producing a three-dimensional image of a cross-section of the body.



Magnetic Resonance

Like CT scans, Magnetic Resonance Imaging (MRI) allows radiologists to see inside the human body without making an incision. Instead of X-rays, MRI scanners use magnetic energy and radio waves to "see" inside the body. The central component of a standard MRI device is a large cylinder-shaped magnet. To take a scan, a patient lies flat inside the device, and the machine sends pulses of powerful radio waves through the body. In response, the atoms that make up the body's tissue vibrate slightly, sending out radio waves of their own. The scanner picks up the body's signals, and—from information based on the strength and location of the signals—a computer translates the signals into a picture. Compared to CT scans or other imaging techniques, MRI produces very detailed images of the body's soft tissues.



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